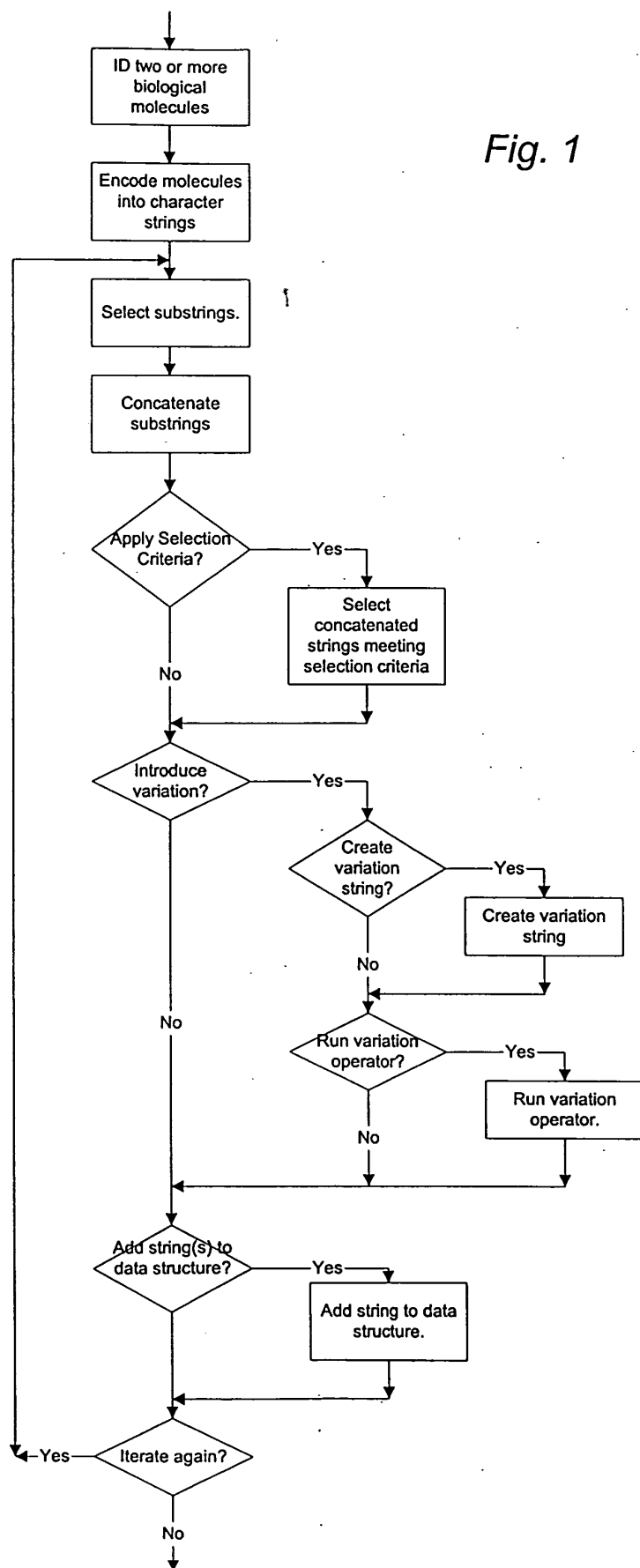


Fig. 1



3271.002US0

Initial strings A, B, and C:

String A: A1 - A2 - A3 - A4 - A5
 String B: B1 - B2 - B3 - B4 - B5
 String C: C1 - C2 - C3 - C4 - C5

Select substrings

String Pools:

Pool 1: A1, B1, C1
 Pool 2: A2, B2, C2
 Pool 3: A3, B3, C3

Concatenate
substrings

New Strings:

String A: A1 - B2 - B3 - C4 - A5
 String B: B1 - C2 - C3 - B4 - B5
 String C: C1 - A2 - A3 - A4 - C5

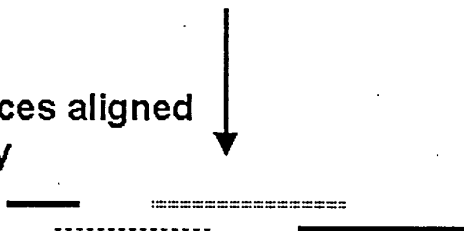
Fig. 2

3271.002WO0

Initial sequences



**Subsequences aligned
by similarity**



**Concatenated
subsequences**

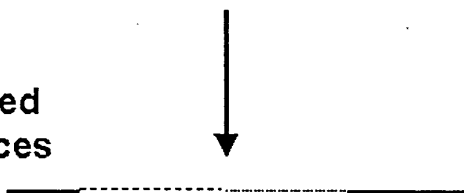


Fig. 3

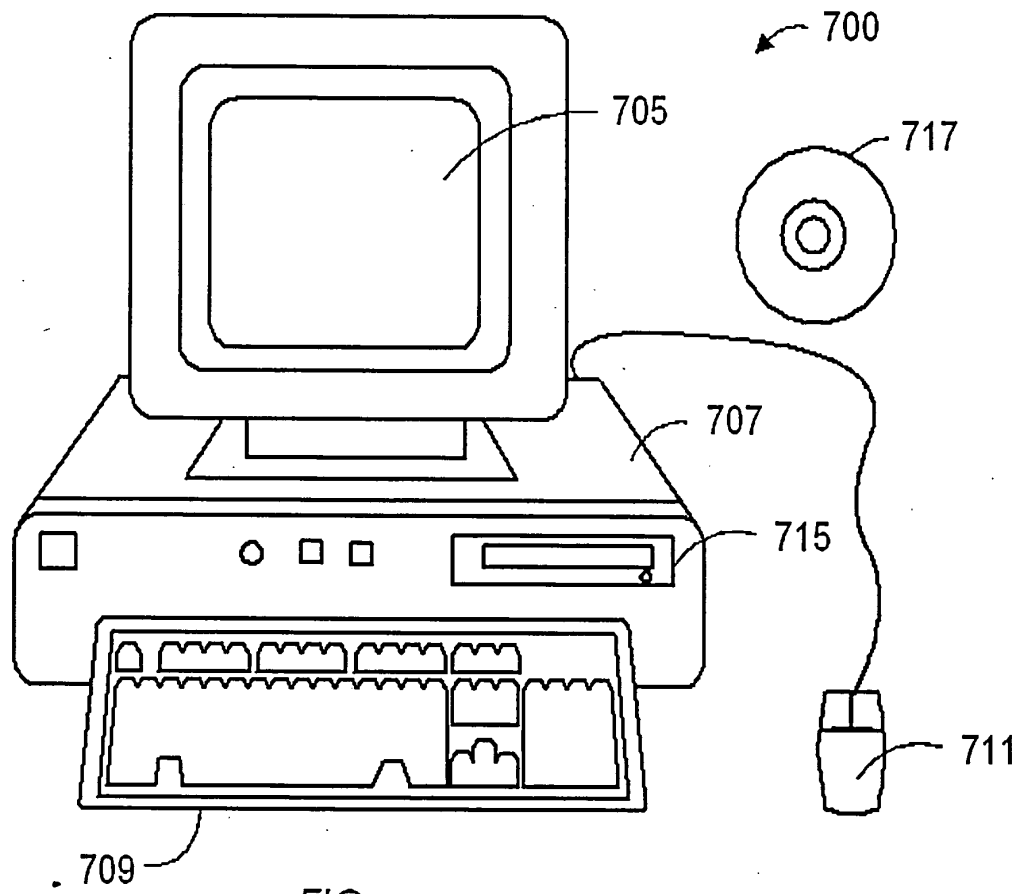


FIG. _____

Fig. 4

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Fig. 5

FAMILY GAGGS MODEL # 1.

SUBTILISIN BACKGROUND INFORMATION:

7 PARENTS, SERINE PROTEASES, DIVERSE

TYPE OF ALIGNMENT/SIMILARITY DATA PRESENTED:
AMINOACID SEQUENCES, LEADER PEPTIDE EXCLUDED.

Percent Similarity

	1	2	3	4	5	6	7	
1	■	62.1	81.4	57.6	81.8	56.1	59.1	1
2	50.5	■	61.0	54.9	59.5	58.2	60.8	2
3	21.0	52.0	■	54.6	78.4	50.6	53.2	3
4	54.4	63.3	62.3	■	52.0	64.6	67.9	4
5	20.5	54.9	25.1	65.6	■	53.9	56.5	5
6	58.6	56.6	72.2	44.2	63.4	■	94.9	6
7	52.5	51.4	66.0	38.5	57.8	4.9	■	7
	1	2	3	4	5	6	7	

A27211 synthetic 309.PM

BACAPRQ subtilisin.PM

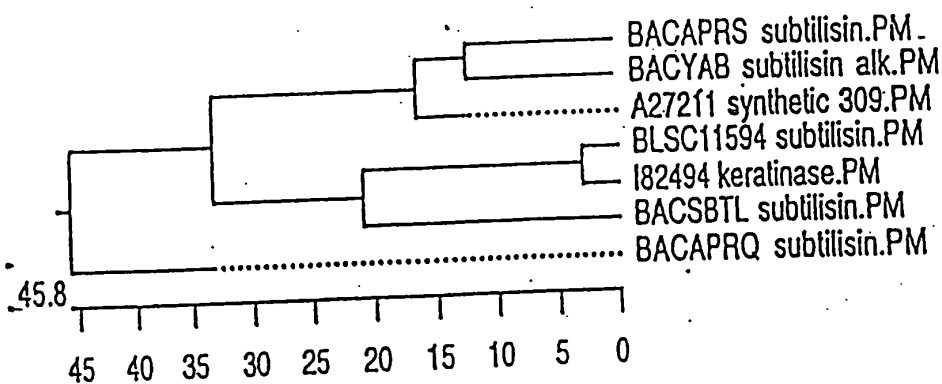
BACAPRS subtilisin.PM

BACSBTL subtilisin.PM

BACYAB subtilisin alk.PM

BLSC11594 subtilisin.PM

I82494 keratinase.PM



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Fig. 6

FAMILY GAGGS: SUBTILISIN MODEL: PAIRWISE DOT-PLOT ALIGNMENTS TO FIND HOMOLOGY AREAS

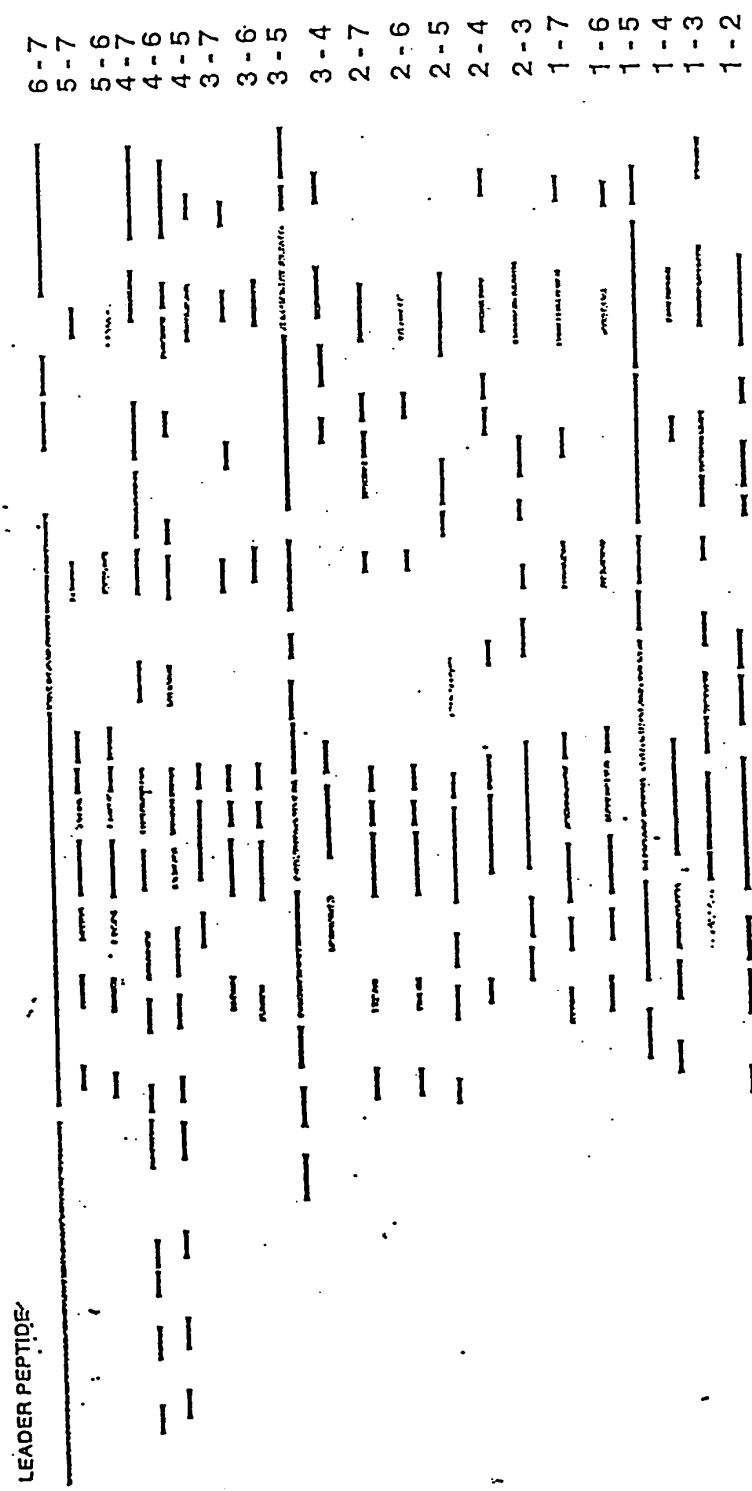


Fig. 7

GAGGS - SUBTILISIN MODEL (7 PARENTS)
SELECTING PAIRWISE CROSSOVER POINTS

